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OM nucleic - nucleic search, using sw model

Run on: June 1, 2003, 18:47:00 ; Search time 5614 Seconds  
(without alignments)  
11570.620 Million cell updates/sec

Title: US-09-625-573-1  
Perfect score: 2232  
Sequence: 1 GGATTGAACAAGGACGCAATT.....TATACTATGTTGATAAAG 2232

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg.hum.\*
- 31: em.htg.inv.\*
- 32: em.htg.other.\*
- 33: em.htg.mus.\*
- 34: em.htg.pin.\*
- 35: em.htg.rod.\*
- 36: em.htg.mam.\*
- 37: em.htg.vrt.\*
- 38: em.sy.\*
- 39: em.htgo.hum.\*
- 40: em.htgo.mus.\*
- 41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description        |
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| 1          | 2232  | 100.0         | 2232   | 6     | AR116074           |
| 2          | 2232  | 100.0         | 2232   | 6     | I79542 Sequence 1  |
| 3          | 2232  | 100.0         | 2232   | 9     | U03882 Human monoc |
| 4          | 1254  | 56.2          | 5471   | 9     | U0924 Human monoc  |
| 5          | 1152  | 51.6          | 143068 | 6     | AX335952 Sequence  |
| 6          | 1152  | 51.6          | 143068 | 9     | U95626 Homo sapien |
| 7          | 1101  | 49.3          | 185437 | 9     | AC098613 Homo sapi |
| 8          | 1068  | 47.8          | 1068   | 11    | G07239 human STS W |
| 9          | 980   | 43.9          | 1979   | 6     | AR116075           |
| 10         | 980   | 43.9          | 1979   | 6     | I79543 Sequence 3  |
| 11         | 980   | 43.9          | 1979   | 9     | U03905 Human monoc |
| 12         | 941   | 42.2          | 1083   | 6     | AX232508 Sequence  |
| 13         | 890   | 39.9          | 1083   | 6     | AX232506 Sequence  |
| 14         | 890   | 39.9          | 1083   | 6     | AX232506 Sequence  |
| 15         | 839   | 37.6          | 1083   | 6     | D29984 Human mRNA  |
| 16         | 839   | 37.6          | 1083   | 6     | AX280849 Sequence  |
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| 18         | 281   | 12.6          | 1651   | 9     | HSMP19EC           |
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| 25         | 77    | 3.4           | 1019   | 9     | AF161925           |
| 26         | 77    | 3.4           | 1019   | 9     | AF161926           |
| 27         | 77    | 3.4           | 1019   | 9     | AF161927           |
| 28         | 77    | 3.4           | 1019   | 9     | AF161928           |
| 29         | 77    | 3.4           | 1019   | 9     | AF161929           |
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| 40         | 65    | 2.9           | 1019   | 9     | AF161901           |
| 41         | 65    | 2.9           | 1019   | 9     | AF161903           |
| 42         | 65    | 2.9           | 1019   | 9     | AF161904           |
| 43         | 65    | 2.9           | 1019   | 9     | AF161905           |
| 44         | 65    | 2.9           | 1019   | 9     | AF161909           |
| 45         | 65    | 2.9           | 1019   | 9     | AF161910           |

ALIGNMENTS

|            |  |             |     |        |                 |
|------------|--|-------------|-----|--------|-----------------|
| RESULT 1   | AR116074   | 2232 bp     | DNA | linear | PAT 16-MAY-2001 |
| LOCUS      | AR116074   | 2232 bp     | DNA | linear | PAT 16-MAY-2001 |
| DEFINITION | Sequence 1 from patent US 6132987.                           |             |     |        |                 |
| ACCESSION  | AR116074   |             |     |        |                 |
| VERSION    | AR116074.1   | GI:14096396 |     |        |                 |
| KEYWORDS   | Unknown.   |             |     |        |                 |
| SOURCE     | Unknown.   |             |     |        |                 |
| ORGANISM   | Unclassified.  |             |     |        |                 |
| REFERENCE  | 1 (bases 1 to 2232)  |             |     |        |                 |
| AUTHORS    | Charo,I.F. and Coughlin,S.R.                                 |             |     |        |                 |
| TITLE      | Recombinant mammalian monocyte chemotactic protein-1 (MCP-1) |             |     |        |                 |
| JOURNAL    | receptors (MCP-1R, CCR-2)                                    |             |     |        |                 |
|            | Patent: US 6132987-A 1 17-OCT-2000;                          |             |     |        |                 |





QY 1561 AGGAGTTGGAAGTGTGATCTGTGGGCACATTAGCCCTATGTGATGCGATGAGTCAAGTA 1620  
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 Db 2221 TGGTATAAAG 2232  
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 HSU03882 2232 bp mRNA linear PRI 22-JUN-1994  
 LOCUS Human monocyte chemoattractant protein 1 receptor (MCP-1RA)  
 DEFINITION alternatively spliced mRNA, complete cds.  
 ACCESSION U03882  
 VERSION U03882.1 GI:472555  
 KEYWORDS human.  
 SOURCE Homo sapiens  
 ORGANISM Human  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2232)  
 AUTHORS Charo, I.F., Myers, S.J., Herman, A., Franci, C., Connolly, A.J. and Coughlin, S.R.  
 TITLE Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternative splicing of the carboxyl-terminal tails  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (7), 2752-2756 (1994)  
 MEDLINE 94195821  
 PUBLISHED 8146186  
 REFERENCE 2 (bases 1 to 2232)  
 AUTHORS Myers, S.J.  
 TITLE Direct Submission

JOURNAL Submitted (01-DEC-1993) Scott J. Myers, Cardiovascular, The Gladstone Institutes, 2550 23rd Street, San Francisco, CA 94110, USA  
 FEATURES source  
 Location/Qualifiers  
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ORIGIN

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QY 2179 TTTAACAACACTGATTTGGAAAAATAAATCAATGCTTAACTATGTTGATAAAG 2232  
Db 4954 TTTAACAACACTGATTTGGAAAAATAAATCAATGCTTAACTATGTTGATAAAG 5007

RESULT 5  
LOCUS AX335952  
DEFINITION Sequence 6461 from Patent WO0194629.  
ACCESSION AX335952  
VERSION AX335952.1 GI:18126671  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,  
Hortigan, S., Soppet, D. R. and Weaver, Z.  
TITLE Cancer gene determination and therapeutic screening using signature  
gene sets  
JOURNAL Patent: WO 0194629-A 6461 13-DEC-2001;  
FEATURES  
Location/Qualifiers  
1. .143068  
/organism="Homo sapiens"









|           |  |             |
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| SOURCE    | human.   |             |
| ORGANISM  | Homo sapiens   |             |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.   |             |
| AUTHORS   | 1 (bases 1 to 185437)<br>Kaul, R. K., Olson, M. V., Zhou, Y., James, R. A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K. A., Buckley, D., Kibukawa, M., Raymond, C. and Haugen, E. D.   |             |
| TITLE     | Direct Submission  |             |
| JOURNAL   | Unpublished  |             |
| REFERENCE | 2 (bases 1 to 185437)<br>Kaul, R. K., Olson, M. V., Raymond, C. and Haugen, E. D.  |             |
| AUTHORS   | Direct Submission  |             |
| TITLE     | Submitted (26-OCT-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA  |             |
| JOURNAL   | 3 (bases 1 to 185437)<br>Kaul, R. K., Olson, M. V., Zhou, Y., James, R. A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K. A., Buckley, D., Kibukawa, M., Raymond, C. and Haugen, E. D.   |             |
| REFERENCE | Direct Submission  |             |
| AUTHORS   | Submitted (01-AUG-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA  |             |
| TITLE     | On Aug 1, 2002 this sequence version replaced gi:16445164.   |             |
| JOURNAL   | ----- Genome Center -----  |             |
| COMMENT   | Center: University of Washington Genome Center<br>Center Code: UWGC<br>Web site: http://www.genome.washington.edu<br>Contact: uwgchgs@u.washington.edu<br>----- Project Information -----<br>Center project name: chr-3<br>Center clone name: RP11-24F11 (bc0137)<br>----- Summary Statistics -----<br>Sequencing vector: plasmid; L08752; 100% of reads<br>Chemistry: Dye-terminator ET; 93% of reads<br>Chemistry: Dye-terminator Big Dye; 7% of reads<br>Assembly program: Phrap; version 0.990319<br>Consensus quality: 184860 bases at least Q40<br>Consensus quality: 185398 bases at least Q30<br>Consensus quality: 185435 bases at least Q20<br>Insert size: 185437; sum-of-contigs<br>Quality coverage: 7.6x in Q20 bases; sum-of-contigs<br>-----<br>Overlapping Sequences:<br>5': BAC-110P12 U95626, 111014-bp overlap<br>3': RP11-509121 (UWGC:bc0454) AC104304, 61294-bp overlap<br>-----<br>Sequence Quality Assessment:<br>This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.<br>All manually edited bases have been reduced to quality zero.<br>Quality levels above 40 are expected to have less than 1 error in 10,000 bp.<br>Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.<br>-----<br>This sequence was finished as follows unless otherwise noted:<br>all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.<br>-----<br>Sequence Validation:<br>This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below.<br>The electronically digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. |             |

Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

| BgIII     |         |           |         | EcoRI     |         |           |         | HindIII   |         |           |         |
|-----------|---------|-----------|---------|-----------|---------|-----------|---------|-----------|---------|-----------|---------|
| SeqDerMap | FngPrnt | SeqDerMap | FngPrnt | SeqDerMap | FngPrnt | SeqDerMap | FngPrnt | SeqDerMap | FngPrnt | SeqDerMap | FngPrnt |
| 11786     | 12040   | 8696      | 8837    | 9531      | 9423    | 9531      | 9423    | 9531      | 9423    | 9531      | 9423    |
| 2067      | 2065    | 6         | <800    | 6382      | 6501    | 6382      | 6501    | 6382      | 6501    | 6382      | 6501    |
| 5681      | 5720    | 1846      | 1824    | 512       | <800    | 512       | <800    | 512       | <800    | 512       | <800    |
| 3716      | 3953    | 4052      | 3986    | 449       | <800    | 449       | <800    | 449       | <800    | 449       | <800    |
| 875       | 897     | 1159      | 1130    | 6692      | 6501    | 6692      | 6501    | 6692      | 6501    | 6692      | 6501    |
| 910       | 897     | 54        | <800    | 10449     | 10229   | 10449     | 10229   | 10449     | 10229   | 10449     | 10229   |
| 2169      | 2215    | 560       | <800    | 953       | 1025    | 953       | 1025    | 953       | 1025    | 953       | 1025    |
| 1705      | 1653    | 2287      | 2267    | 3124      | 3176    | 3124      | 3176    | 3124      | 3176    | 3124      | 3176    |
| 5763      | 5720    | 4905      | 4891    | 1054      | 1025    | 1054      | 1025    | 1054      | 1025    | 1054      | 1025    |
| 5844      | 5720    | 3049      | 3078    | 3985      | 3998    | 3985      | 3998    | 3985      | 3998    | 3985      | 3998    |
| 5061      | 5001    | 1377      | 1394    | 1100      | 1025    | 1100      | 1025    | 1100      | 1025    | 1100      | 1025    |
| 2625      | 2640    | 9903      | 9772    | 124       | <800    | 124       | <800    | 124       | <800    | 124       | <800    |
| 725       | <800    | 1022      | 1021    | 2671      | 2693    | 2671      | 2693    | 2671      | 2693    | 2671      | 2693    |
| 1173      | 1161    | 12606     | 12503   | 1948      | 1968    | 1948      | 1968    | 1948      | 1968    | 1948      | 1968    |
| 5747      | 5720    | 866       | 868     | 83        | <800    | 83        | <800    | 83        | <800    | 83        | <800    |
| 9995      | 9684    | 9817      | 9772    | 7455      | 7474    | 7455      | 7474    | 7455      | 7474    | 7455      | 7474    |
| 999       | 999     | 3598      | 3601    | 1305      | 1267    | 1305      | 1267    | 1305      | 1267    | 1305      | 1267    |
| 4541      | 4503    | 452       | <800    | 1047      | 1025    | 1047      | 1025    | 1047      | 1025    | 1047      | 1025    |
| 2950      | 2981    | 7549      | 7635    | 3299      | 3301    | 3299      | 3301    | 3299      | 3301    | 3299      | 3301    |
| 406       | <800    | 2063      | 2075    | 5279      | 5237    | 5279      | 5237    | 5279      | 5237    | 5279      | 5237    |
| 3375      | 3602    | 5837      | 5858    | 6815      | 6926    | 6815      | 6926    | 6815      | 6926    | 6815      | 6926    |
| 13024     | 13045   | 13685     | 13328   | 435       | <800    | 435       | <800    | 435       | <800    | 435       | <800    |
| 416       | <800    | 4104      | 3986    | 2509      | 2576    | 2509      | 2576    | 2509      | 2576    | 2509      | 2576    |
| 10298     | 10140   | 1943      | 1928    | 2218      | 2172    | 2218      | 2172    | 2218      | 2172    | 2218      | 2172    |
| 1478      | 1452    | 3964      | 3986    | 3797      | 3802    | 3797      | 3802    | 3797      | 3802    | 3797      | 3802    |
| 287       | <800    | 2758      | 2771    | 7758      | 7830    | 7758      | 7830    | 7758      | 7830    | 7758      | 7830    |
| 205       | <800    | 167       | <800    | 16192     | 16442   | 16192     | 16442   | 16192     | 16442   | 16192     | 16442   |
| 9428      | 9684    | 1307      | 1304    | 11020     | 10820   | 11020     | 10820   | 11020     | 10820   | 11020     | 10820   |
| 3809      | 3953    | 13306     | 13328   | 1978      | 1968    | 1978      | 1968    | 1978      | 1968    | 1978      | 1968    |
| 1275      | 1234    | 2423      | 2450    | 8741      | 8681    | 8741      | 8681    | 8741      | 8681    | 8741      | 8681    |
| 3351      | 3381    | 2243      | 2267    | 4795      | 4815    | 4795      | 4815    | 4795      | 4815    | 4795      | 4815    |

## FEATURES

source  
location/Qualifiers  
1..185437  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="3"  
/clone="RP11-24F11"

Query Match 49.3%; Score 1101; DB 9; Length 185437;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1251; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 979 AGCCTTTTTCACATAGCTCTGGCTGTAGGATGCCCCACCTCCAAAACCAAGTGTGGA 1038  
Db 16204 AGCCTTTTTCACATAGCTCTGGCTGTAGGATGCCCCACCTCCAAAACCAAGTGTGGA 16263  
QY 1039 GGTCCAGAGTGACAGAGAAAGAAATGTGAAAGTGACTACACAGGACTCTCGATGGT 1098  
Db 16264 GGTCCAGAGTGACAGAGAAAGAAATGTGAAAGTGACTACACAGGACTCTCGATGGT 16323  
QY 1099 CGTGGAAAAGAAAGTCAATTGGCAGAGCCCTGAAGCCAGTCTTCAGACAAAGAGA 1158  
Db 16324 CGTGGAAAAGAAAGTCAATTGGCAGAGCCCTGAAGCCAGTCTTCAGACAAAGAGA 16383  
QY 1159 GCTAGACAGAAATGACAGATCTCTGCTTTGGAAATCACACGCTTGCAGATG 1218  
Db 16384 GCTAGACAGAAATGACAGATCTCTGCTTTGGAAATCACACGCTTGCAGATG 16443

|            |  |  |       |
|------------|--|--|-------|
| QY         | 1219                                     | TGCTATTCACAGTGTGAATCTTGGTGTCTACGTTTACAGGAGGAGGCTCAGAGGAG       | 1278  |
| Db         | 16444                                    | TGTGATTCACAGTGTGAATCTTGGTGTCTACGTTTACAGGAGGAGGCTCAGAGGAG       | 16503 |
| QY         | 1279                                     | AGACTCCAGCTGGGTGGAAACAGTATTTCCAACTACCTTCAGTTCCTCAATTTTG        | 1338  |
| Db         | 16504                                    | AGACTCCAGCTGGGTGGAAACAGTATTTCCAACTACCTTCAGTTCCTCAATTTTG        | 16563 |
| QY         | 1339                                     | AATCAGGATAGAGTTTCCAGACTTTTAAATAGTAAATAAATAAAGCTCAAAAC          | 1398  |
| Db         | 16564                                    | AATCAGGATAGAGTTTCCAGACTTTTAAATAGTAAATAAATAAAGCTCAAAAC          | 16623 |
| QY         | 1399                                     | TGCACTTTGTAATCTGTGTAAGAGTTAGTTTGGTTCATCATCTCAAAAGCTGAAAT       | 1458  |
| Db         | 16624                                    | TGCACTTTGTAATCTGTGTAAGAGTTAGTTTGGTTCATCATCTCAAAAGCTGAAAT       | 16683 |
| QY         | 1459                                     | GCTGATTTAGTCACAGAGATAATCTAGCTTTGAGCTTAAGAAATTTGAGCAGGTGGTAT    | 1518  |
| Db         | 16684                                    | GCTGATTTAGTCACAGAGATAATCTAGCTTTGAGCTTAAGAAATTTGAGCAGGTGGTAT    | 16743 |
| QY         | 1519                                     | GTTTGGGAGCTGCTGAGTCAACCAATAGTTTGGTTCAGGAGTTGGAAGTGTGTG         | 1578  |
| Db         | 16744                                    | GTTTGGGAGCTGCTGAGTCAACCAATAGTTTGGTTCAGGAGTTGGAAGTGTGTG         | 16803 |
| QY         | 1579                                     | ATCTGTGGCAGATTTAGCCTATGTGCATGAGCATCTAAGTAAATGATGCTTTGAATCA     | 1638  |
| Db         | 16804                                    | ATCTGTGGCAGATTTAGCCTATGTGCATGAGCATCTAAGTAAATGATGCTTTGAATCA     | 16863 |
| QY         | 1639                                     | CAGTATACGCTCCATCGCTGTCATCTCAGCTGATCTCTCAGGCTTGTGCGCA           | 1698  |
| Db         | 16864                                    | CAGTATACGCTCCATCGCTGTCATCTCAGCTGATCTCTCAGGCTTGTGCGCA           | 16923 |
| QY         | 1699                                     | AAAGCCTTTTGTGTTTGTGTTTATCATATTAAGTCAATGCGTTTAAATCAATTCGAGT     | 1758  |
| Db         | 16924                                    | AAAGCCTTTTGTGTTTGTGTTTATCATATTAAGTCAATGCGTTTAAATCAATTCGAGT     | 16983 |
| QY         | 1759                                     | GTTTCAGTGTGCGAGATGCTTGTGATGCTCATATTTGCCCTAATTTGCCAGTGGAA       | 1818  |
| Db         | 16984                                    | GTTTCAGTGTGCGAGATGCTTGTGATGCTCATATTTGCCCTAATTTGCCAGTGGAA       | 17043 |
| QY         | 1819                                     | CTCCTAAATCAAAATTTGGCTTCTAATCAAAAGCTTTTAAACCTTATTTGTAAGAATGGAAG | 1878  |
| Db         | 17044                                    | CTCCTAAATCAAAATTTGGCTTCTAATCAAAAGCTTTTAAACCTTATTTGTAAGAATGGAAG | 17103 |
| QY         | 1879                                     | GTGAGAGCTCCCTGAAGTAAGCAAGACTTTCCCTCTTAGTCAGCCAGTTAAGATG        | 1938  |
| Db         | 17104                                    | GTGAGAGCTCCCTGAAGTAAGCAAGACTTTCCCTCTTAGTCAGCCAGTTAAGATG        | 17163 |
| QY         | 1939                                     | TTCTTATTTGCCAGTGTGTTTCTGATCTGATCAAGCAAGAAACACTGGGCTTCTAGA      | 1998  |
| Db         | 17164                                    | TTCTTATTTGCCAGTGTGTTTCTGATCTGATCAAGCAAGAAACACTGGGCTTCTAGA      | 17223 |
| QY         | 1999                                     | ACCAGGCAACTTGGGAAGTACACTCCCAAGCTGGAGTATGCTCTACTTTTCAGGCCACAT   | 2058  |
| Db         | 17224                                    | ACCAGGCAACTTGGGAAGTACACTCCCAAGCTGGAGTATGCTCTACTTTTCAGGCCACAT   | 17283 |
| QY         | 2059                                     | GGCTAAAGAGGTTTCAGAAAGAGTGGGAGCAGAGCAAGTTCACCTTCATATATTT        | 2118  |
| Db         | 17284                                    | GGCTAAAGAGGTTTCAGAAAGAGTGGGAGCAGAGCAAGTTCACCTTCATATATTT        | 17343 |
| QY         | 2119                                     | GTATGATCCTTAATGAATCAATAAATGTTAAGTTGATGGTGAATGTAATACTGTT        | 2178  |
| Db         | 17344                                    | GTATGATCCTTAATGAATCAATAAATGTTAAGTTGATGGTGAATGTAATACTGTT        | 17403 |
| QY         | 2179                                     | TTTAACTACTATGTTTGGAAATAAATCAATGCTATTAATGTTGTAAGAAG             | 2232  |
| Db         | 17404                                    | TTTAACTACTATGTTTGGAAATAAATCAATGCTATTAATGTTGTAAGAAG             | 17457 |
| RESULT     | 8  |  |       |
| G07239     |  |  |       |
| LOCUS      |  |  |       |
| DEFINITION | human STS WI-9314, sequence tagged site. |  |       |

|           |   |
|-----------|---|
| ACCESSION | G07239  |
| VERSION   | G07239.1  |
| KEYWORDS  | GI:860484   |
| SOURCE    | STS; STS sequence; primer; sequence tagged site.  |
|           | Homo sapiens STSs derived from sequences in dbEST and the Unigene collection.   |
| ORGANISM  | Homo sapiens  |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  |
| AUTHORS   | 1 (bases 1 to 1068)   |
| TITLE     | Hudson,T. Whitehead Institute/MIT Center for Genome Research; Physically Mapped ESTs  |
| JOURNAL   | Unpublished (1995)  |
| COMMENT   | Contact: Thomas Hudson<br>Whitehead Institute/MIT Center for Genome Research<br>Whitehead Institute for Biomedical Research<br>9 Cambridge Center, Cambridge MA 02142 USA<br>Tel: 617 252 1900<br>Fax: 617 252 1902<br>Email: thudson@genome.wi.mit.edu   |
|           | Primer A: GGAATCACAGCTCTGGCTT<br>Primer B: ACTGTTTCCAAACCCAGCTG<br>STS size: 114<br>PCR Profile:<br>Presoak:<br>Denaturation:<br>Annealing: 56 degrees C<br>Polymerization:<br>PCR Cycles: 35<br>Thermal Cycler:<br>Protocol:<br>Template: 10 ng<br>Primer: each 5 pM<br>dNTPs: each 4 mM<br>Taq Polymerase: 0.025 units/ul<br>Total Vol: 20 ul |
|           | Buffer:<br>MgCl2: 1.5 mM<br>KCl: 50 mM<br>Tris-HCL: 10 mM<br>pH: 9.3  |
|           | Prepared with primer pairs derived from U03882 -- Unigene.  |
| FEATURES  | source<br>1..1068<br>Location/Qualifiers<br>/organism="Homo sapiens"<br>/db_xref="taxon:9606"<br>/map="730_D_5; 913_C_5; 941_A_7; 743_H_10; 781_B_10;<br>881_F_10; 881_F_11"<br>27..140<br>27..46<br>primer_bind<br>primer_bind<br>complement(121..140)<br>BASE COUNT<br>315 a 186 c 238 g 329 t  |
| ORIGIN    |   |
|           | Query Match 47.8%; Score 1068; DB 11; Length 1068;<br>Best Local Similarity 100.0%; Pred. No. 0;<br>Matches 1068; Conservative 0; Mismatches 0; Indels 0; Gaps 0;   |
| Qy        | 1165 AGACAGAAATGACAGATCTCTGCTTTGGAAATCACACGCTCGGCTTCACAGATGTGAT 1224<br>     <br>   |
| Db        | 1 AGACAGAAATGACAGATCTCTGCTTTGGAAATCACACGCTCGGCTTCACAGATGTGAT 60<br>     <br>  |
| Qy        | 1225 TCACAGTGTGAATCTTGGTGTCTAGTTACCAGGCAGGAAGGCTGAGAGGAGAGACTC 1284<br>     <br>  |
| Db        | 61 TCACAGTGTGAATCTTGGTGTCTAGTTACCAGGCAGGAAGGCTGAGAGGAGAGACTC 120<br>     <br>   |
| Qy        | 1285 CAGCTGGGTGGAAACAGATATTTTCCAACTACCTTCAGTTCCTCATTTTGAATACA 1344<br>     <br>   |
| Db        | 121 CAGCTGGGTGGAAACAGATATTTTCCAACTACCTTCAGTTCCTCATTTTGAATACA 180<br>     <br>   |





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BASE COUNT 530 a 435 c 451 g 563 t  
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Query Match 43.9%; Score 980; DB 9; Length 1979;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAGTCAACACCTTTTGTATGAT 120  
DB 102 CGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAGTCAACACCTTTTGTATGAT 161  
QY 121 TAGGCTGCTCCCTGTCAATATTTGACGTGAAGCAAAATGGGCGCCAACTCCTGCCTCG 180  
DB 162 TAGGCTGCTCCCTGTCAATATTTGACGTGAAGCAAAATGGGCGCCAACTCCTGCCTCG 221  
QY 181 CTCTACTCGCTGGTGTCTATCTTTGTTTGGGCAACATGCTGGTCTCTCATCTTA 240  
DB 222 CTCTACTCGCTGGTGTCTATCTTTGTTTGGGCAACATGCTGGTCTCTCATCTTA 281  
QY 241 ATAACTGCAAAAGCTGAAGTCTGTACTGTACATTTACTCTCAACCTGGCCATCTCT 300  
DB 282 ATAACTGCAAAAGCTGAAGTCTGTACTGTACATTTACTCTCAACCTGGCCATCTCT 341  
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DB 342 GATCTGCTTTTCTTACTCTCCCATGTTGGGCTCACTCTGCTGCAATGAGTGGTC 401  
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QY 421 ATCTTCTTCATCATCTCTGCAATGATAGATACCTGGCTATTTGCTCATGCTGTT 480  
DB 462 ATCTTCTTCATCATCTCTGCAATGATAGATACCTGGCTATTTGCTCATGCTGTT 521  
QY 481 GCTTTAAAGCCAGACGCTCACCTTTGGGCTGTGCAAGTGTGATCACCTGGTGGTG 540  
DB 522 GCTTTAAAGCCAGACGCTCACCTTTGGGCTGTGCAAGTGTGATCACCTGGTGGTG 581  
QY 541 GCTGTGTTGCTCTGTCGCCAGGAATCATCTTTACTAAATGCCAGAAAGATTTCTGT 600  
DB 582 GCTGTGTTGCTCTGTCGCCAGGAATCATCTTTACTAAATGCCAGAAAGATTTCTGT 641  
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QY 661 ATTTGGGCTGTGTCCTGCTCATGCTGCTCATGCTGCTGCTGCTGCTGCTGCTGCT 720  
DB 702 ATTTGGGCTGTGTCCTGCTCATGCTGCTCATGCTGCTGCTGCTGCTGCTGCTGCT 761  
QY 721 ACCCTGCTGCTGTCGAAACGAGAGAGGATAGGCGAGTGGAGTGCATCTTCAAC 780  
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QY 781 ATCATGATTTTCTCTTCTGACTCCCTATATACATTTGATCTCTCTGACACAC 840  
DB 822 ATCATGATTTTCTCTTCTGACTCCCTATATACATTTGATCTCTCTGACACAC 881  
QY 841 TTCCAGGAATTTCTGCGCTGAGTAACTGTGAAGCACCAGTCACTGGACCAAGCAG 900  
DB 882 TTCCAGGAATTTCTGCGCTGAGTAACTGTGAAGCACCAGTCACTGGACCAAGCAG 941

QY 901 CAGGTGACAGAGACTTTGGGATGACTCAGTCTGCATCAATCCCATCATCTATGCTTC 960  
DB 942 CAGGTGACAGAGACTTTGGGATGACTCAGTCTGCATCAATCCCATCATCTATGCTTC 1001  
QY 961 GTTGGGGAGAAAGTTCAGAAG 980  
DB 1002 GTTGGGGAGAAAGTTCAGAAG 1021

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LOCUS AX232508 1083 bp DNA linear PAT 11-SEP-2001  
DEFINITION Sequence 3 from Patent WO0162796.  
ACCESSION AX232508  
VERSION AX232508.1 GI:15592570  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1083)  
AUTHORS Valdes, A.M., Groot, P.H. and Spurr, N.K.  
TITLE Ccr2-64i, polymorphic variant of the human cor2 receptor and its  
use in the diagnostic and treatment of atherosclerosis  
JOURNAL Patent: WO 0162796-A 30-AUG-2001;  
SMITHKLINE BEECHAM PLC (GB)  
FEATURES  
Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 255 a 260 c 247 g 321 t  
ORIGIN

Query Match 42.2%; Score 941; DB 6; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 941; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 ATGCTGTCCACATCTGTTCTCGGTTATTCAGAAATACCAAGAGAGCGGTGAAGAATC 99  
DB 1 ATGCTGTCCACATCTGTTCTCGGTTATTCAGAAATACCAAGAGAGCGGTGAAGAATC 60  
QY 100 ACCACCTTTTGTATGATTACGCTGCTCCCTGTGCATAAATTCACCTGAAGCAAT 159  
DB 61 ACCACCTTTTGTATGATTACGCTGCTCCCTGTGCATAAATTCACCTGAAGCAAT 120  
QY 160 GGGCCCCAATCCTGCTCCGCTCTACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 219  
DB 121 GGGCCCCAATCCTGCTCCGCTCTACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
QY 220 ATGCTGTGCTCCTCATCTTAATAAAGTCAAAAGCTGAAGTCTGCTGCTGCTGCTGCT 279  
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DB 241 CTGCTCAACCTGGCCATCTGATCTGCTTTTCTTATTAATCTCCCATTTGGGCTCAC 300  
QY 340 TCTGCTGCAATGAGTGGTCTTTGGGAATGCAATGTCGAATATTTACAGAGGCTGAT 399  
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DB 361 CACATCGGTTATTTGGCGGAATCTTCTTCATCATCTCTCTGCAATGATAGATACCTG 420  
QY 460 GCTATTGTCATGCTGTTTGGTCTTTAAAGCCAGAGCGGTCACTTTGGGTTGGTGACA 519  
DB 421 GCTATTGTCATGCTGTTTGGTCTTTAAAGCCAGAGCGGTCACTTTGGGTTGGTGACA 480  
QY 520 AGTGTGATCACCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 579  
DB 481 AGTGTGATCACCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 540





**AUTHORS**  
**TITLE**  
**JOURNAL**

**COMMENT**

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Direct Submission  
Submitted (22-APR-1994) Shinsuke Yamagami, TEIJIN LIMITED,  
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191, Japan (Tel: 0425-86-8282)  
Submitted (22-APR-1994) to DDBJ by:  
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Institute for Bio-Medical Research  
4-3-2 Asanigaoka  
Hino, Tokyo 191  
Japan  
Phone: 0425-86-8282  
Fax: 0425-87-5512

[illegible]

5

[illegible]

Db 481 AGTGTGATCACCTGGTGTGGCTGTGTTTGTCTTGTGCCAGGAATCATCTTTACTAAA 540

QY 580 TCCAGAAAGAAGATTCGTTTATGTCGTGCGCCCTTATTTTCACGAGGATGGAATAAT 639

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QY 640 TTCACACATAAATAGAGAAACATTTTGGGGCTGGTCCCTGCGCTGCTCATCTGGTGCATC 699

Db 601 TTCACACATAAATAGAGAAACATTTTGGGGCTGGTCCCTGCGCTGCTCATCTGGTGCATC 660

QY 700 TGCTACTCGGGAATCCGTAACCCCTGCTTCGGTGTGTCGAAACGAGAAGAAGAGGCATAGG 759

Db 661 TGCTACTCGGGAATCCGTAACCCCTGCTTCGGTGTGTCGAAACGAGAAGAAGAGGCATAGG 720

QY 760 GCAGTGAGATCATCTTCCACATCATGATGTTTACTTCTCTTCTGGACTCCCTATAAC 819

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RESULT 15

AX280849

LOCUS

DEFINITION

Sequence 472 from Patent WO01/71712.

ACCESSION

AX280849

VERSION

AX280849.1

KEYWORDS

GI:16608180

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

Lehmann-Bruhlma, K., Liaw, C.W. and Lin, I.L.

Non-endogenous, constitutively activated known g protein-coupled receptors

JOURNAL

Patent: WO 01/7172-A 472 18-OCT-2001;

Arena Pharmaceuticals, Inc. (US)

FEATURES

source

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/db\_xref="taxon:9606"

BASE COUNT

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ORIGIN

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Best Local Similarity 99.8%; Pred. No. 0;

Matches 939; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 100 ACCACCTTTTGGATATGATACGATACGGTGCCTCGCTGTCATAAATTTGACGTGAAGCAAAAT 159

Db 61 ACCACCTTTTGGATATGATACGATACGGTGCCTCGCTGTCATAAATTTGACGTGAAGCAAAAT 120

QY 160 GGGGCCAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTCTGGGCAAC 219

Db 121 GGGGCCAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTCTGGGCAAC 180

QY 220 ATGCTGGTGTCTCATCTTAATAACTGCAGAAAAAGCTGAAGTGTGCTGACATTTTAC 279



